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**Genome-wide detection of high abundance N6-methyladenosine sites by microarray.**

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**Public Summary:**

N6-methyladenosine is the most abundant modification on the messenger RNAs of mammalian cells. But there is a lack of technology to detect those modification sites precisely and efficiently. We found N6-methyladenosine can inhibit Watson-Crick pairing between nucleic acids. And based on this discovery we developed a novel method to detect N6-methyladenosine modification through the whole genome transcripts.

**Scientific Abstract:**

N(6)-methyladenosine (m(6)A), the most abundant internal RNA modification, functions in diverse biological processes, including regulation of embryonic stem cell self-renewal and differentiation. As yet, methods to detect m(6)A in the transcriptome rely on the availability and quality of an m(6)A antibody and are often associated with a high rate of false positives. Here, based on our observation that m(6)A interferes with A-T/U pairing, we report a microarray-based technology to map m(6)A sites in mouse embryonic stem cells. We identified 72 unbiased sites exhibiting high m(6)A levels from 66 PolyA RNAs. Bioinformatics analyses suggest identified sites are enriched on developmental regulators and may in some contexts modulate microRNA/mRNA interactions. Overall, we have developed microarray-based technology to capture highly enriched m(6)A sites in the mammalian transcriptome. This method provides an alternative means to identify m(6)A sites for certain applications.

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